

05-9010330

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#7

## RAW SEQUENCE LISTING

DATE: 03/03/2003 p.6

PATENT APPLICATION: US/09/832,189A

TIME: 12:54:19

Input Set : A:\PH-1167US seq-revised.txt

Output Set: N:\CRF4\03032003\I832189A.raw

3 <110> APPLICANT: RIKEN  
 5 <120> TITLE OF INVENTION: Truncated Reelin Protein and DNA Encoding the Same  
 7 <130> FILE REFERENCE: PH-1167  
 9 <140> CURRENT APPLICATION NUMBER: US 09/832,189A  
 10 <141> CURRENT FILING DATE: 2001-04-11  
 12 <150> PRIOR APPLICATION NUMBER: JP 2000-109954  
 13 <151> PRIOR FILING DATE: 2000-04-11  
 15 <160> NUMBER OF SEQ ID NOS: 28  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 2274  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Xenopus laevis  
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 25 <221> NAME/KEY: misc\_feature  
 26 <222> LOCATION: (100)  
 27 <223> OTHER INFORMATION: a or g or t or c  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (157)..(1455)  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: sig\_peptide  
 35 <222> LOCATION: (157)..(234)  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: misc\_feature  
 39 <222> LOCATION: (241)..(726)  
 40 <223> OTHER INFORMATION: F-spondin domain  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: misc\_feature  
 44 <222> LOCATION: (847)..(1197)  
 45 <223> OTHER INFORMATION: CR-50 epitope region  
 47 <400> SEQUENCE: 1  
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 52 atgaagaaAG ctcattaAGA acagtggac ccagGA atG gaa CTG CTC cac acc 174  
 53 Met Glu Leu Leu His Thr  
 54 1 5  
 56 ttc tgc ggt ggg cgc tgg act ttG ctG ctc ttc acG ggg atc ttG tgc 222  
 57 Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu Phe Thr Gly Ile Leu Cys  
 58 10 15 20  
 60 ttt gtt gtt GCC CGC GGA GTG GGG TAT TAT CCC AGG TTC TCT CCA TTC 270  
 61 Phe Val Val Ala Arg Gly Val Gly Tyr Tyr Pro Arg Phe Ser Pro Phe  
 62 25 30 35

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64	ttt	tac	cat	cat	gga	gaa	ctg	gaa	gga	gat	ggg	gaa	caa	318			
65	Phe	Phe	Leu	Cys	Thr	His	His	Gly	Glu	Leu	Glu	Gly	Asp	Gly	Glu	Gln	
66	40.				45					50							
68	gga	gaa	gtg	ctc	atc	tct	ctg	cac	ctg	gcg	ggc	aac	ccc	agc	tac	tac	366
69	Gly	Gly	Val	Leu	Ile	Ser	Leu	His	Leu	Ala	Gly	Asn	Pro	Ser	Tyr	Tyr	
70	55				60					65				70			
72	ata	cct	ggg	cag	gag	tac	cat	gtg	acc	ata	tcc	act	agt	acc	ttc	ttt	414
73	Ile	Pro	Gly	Gln	Glu	Tyr	His	Val	Thr	Ile	Ser	Thr	Ser	Thr	Phe	Phe	
74					75					80				85			
76	gat	ggt	ctt	ctg	gtg	act	gga	ctt	tac	act	tct	acc	agt	gtt	caa	gcg	462
77	Asp	Gly	Leu	Leu	Val	Thr	Gly	Leu	Tyr	Thr	Ser	Thr	Ser	Val	Gln	Ala	
78					90					95				100			
80	tct	cag	agc	att	gga	ggc	tct	aaa	gca	ttt	gga	ttt	ggt	att	atg	agc	510
81	Ser	Gln	Ser	Ile	Gly	Gly	Ser	Lys	Ala	Phe	Gly	Phe	Gly	Ile	Met	Ser	
82					105					110				115			
84	gac	cgt	cag	ttt	ggt	acc	cag	ttt	atg	tgc	agt	gtc	gtt	gct	tcc	cac	558
85	Asp	Arg	Gln	Phe	Gly	Thr	Gln	Phe	Met	Cys	Ser	Val	Val	Ala	Ser	His	
86					120					125				130			
88	gtg	agt	cat	ctt	ccc	aca	aca	aac	cta	agt	ttt	gtt	tgg	att	gca	cca	606
89	Val	Ser	His	Leu	Pro	Thr	Thr	Asn	Leu	Ser	Phe	Val	Trp	Ile	Ala	Pro	
90	135				140					145				150			
92	cca	gca	ggt	aca	gga	tgt	gtc	aac	ttc	atg	gcc	aca	gca	aca	cat	agg	654
93	Pro	Ala	Gly	Thr	Gly	Cys	Val	Asn	Phe	Met	Ala	Thr	Ala	Thr	His	Arg	
94					155					160				165			
96	gga	caa	gtt	att	ttc	aag	gat	gcc	ctg	gca	caa	ctg	tgc	gaa	caa	702	
97	Gly	Gln	Val	Ile	Phe	Lys	Asp	Ala	Leu	Ala	Gln	Gln	Leu	Cys	Glu	Gln	
98					170					175				180			
100	gga	gct	cct	act	gaa	gct	ccc	ttt	cg	cct	aat	tta	gcc	gaa	att	cac	750
101	Gly	Ala	Pro	Thr	Glu	Ala	Pro	Leu	Arg	Pro	Asn	Leu	Ala	Glu	Ile	His	
102					185					190				195			
104	agt	gaa	agc	atc	ctt	tta	cga	gat	gat	ttt	gac	tca	tat	aag	ctt	cag	798
105	Ser	Glu	Ser	Ile	Leu	Leu	Arg	Asp	Asp	Phe	Asp	Ser	Tyr	Lys	Leu	Gln	
106					200					205				210			
108	gaa	ttt	aat	cca	aat	att	tgg	ctc	cag	tgc	aga	aat	tgc	gaa	gtt	ggt	846
109	Glu	Leu	Asn	Pro	Asn	Ile	Trp	Leu	Gln	Cys	Arg	Asn	Cys	Glu	Val	Gly	
110	215				220					225				230			
112	gag	cag	tgt	gca	att	atg	cat	ggt	ggg	gca	gtc	act	ttt	tgt	gat	894	
113	Glu	Gln	Cys	Gly	Ala	Ile	Met	His	Gly	Gly	Ala	Val	Thr	Phe	Cys	Asp	
114					235					240				245			
116	ccg	tat	gga	cca	aga	gaa	ttt	ata	act	gtt	caa	atg	aac	aca	act	acg	942
117	Pro	Tyr	Gly	Pro	Arg	Glu	Leu	Ile	Thr	Val	Gln	Met	Asn	Thr	Thr	Thr	
118					250					255				260			
120	gca	tct	gtt	ttt	cag	ttt	tct	att	ggg	tca	gga	tgc	tgc	agg	ttc	agc	990
121	Ala	Ser	Val	Leu	Gln	Phe	Ser	Ile	Gly	Ser	Gly	Ser	Cys	Arg	Phe	Ser	
122					265					270				275			
124	tat	tca	gac	cct	gga	att	gtt	gtt	tca	tac	aca	aag	aat	aat	tca	tct	1038
125	Tyr	Ser	Asp	Pro	Gly	Ile	Val	Val	Ser	Tyr	Thr	Lys	Asn	Asn	Ser	Ser	
126					280					285				290			
128	agt	tgg	atg	cca	ttt	gag	aga	att	agt	gct	cct	tcc	aat	gtt	agc	acc	1086

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Input Set : A:\PH-1167US seq-revised.txt  
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129	Ser	Trp	Met	Pro	Leu	Glu	Arg	Ile	Ser	Ala	Pro	Ser	Asn	Val	Ser	Thr	
130	295				300											310	
132	atc	att	cac	att	att	tac	cta	cct	cct	gaa	gct	aaa	gga	gaa	aat	gtg	1134
133	Ile	Ile	His	Ile	Ile	Tyr	Leu	Pro	Pro	Glu	Ala	Lys	Gly	Glu	Asn	Val	
134					315					320						325	
136	aaa	ttc	cgt	tgg	agg	cag	gag	aac	atg	cag	gca	ggt	gat	gtg	tat	gaa	1182
137	Lys	Phe	Arg	Trp	Arg	Gln	Glu	Asn	Met	Gln	Ala	Gly	Asp	Val	Tyr	Glu	
138					330					335						340	
140	gcc	tgc	tgg	gca	ctg	gat	aac	att	ttg	att	atc	aat	gct	gct	cat	aaa	1230
141	Ala	Cys	Trp	Ala	Leu	Asp	Asn	Ile	Leu	Ile	Ile	Asn	Ala	Ala	His	Lys	
142					345					350						355	
144	gaa	gtc	gtg	tta	gaa	gac	aat	cta	gat	cca	atg	gac	aca	gga	aac	tgg	1278
145	Glu	Val	Val	Leu	Glu	Asp	Asn	Leu	Asp	Pro	Met	Asp	Thr	Gly	Asn	Trp	
146					360					365						370	
148	ctt	ttt	tcc	ggg	gct	act	gta	aag	cat	acc	tgt	cag	tcg	gat	gga		1326
149	Leu	Phe	Phe	Pro	Gly	Ala	Thr	Val	Lys	His	Thr	Cys	Gln	Ser	Asp	Gly	
150					375					380						390	
152	aac	tct	ata	tat	ttt	cat	ggc	aca	gaa	agc	agt	gaa	tac	aac	ttt	gct	1374
153	Asn	Ser	Ile	Tyr	Phe	His	Gly	Thr	Glu	Ser	Ser	Glu	Tyr	Asn	Phe	Ala	
154					395					400						405	
156	act	acc	aga	gat	gtg	gat	ctt	tcc	agt	gag	gac	atc	cag	gac	cag	tgg	1422
157	Thr	Thr	Arg	Asp	Val	Asp	Leu	Ser	Ser	Glu	Asp	Ile	Gln	Asp	Gln	Trp	
158					410					415						420	
160	tct	gaa	gag	ttt	gag	aat	cta	cca	gct	ggg	taa	attttagatg	tagccatgag			1475	
161	Ser	Glu	Glu	Phe	Glu	Asn	Leu	Pro	Ala	Gly							
162					425					430							
164	cattacattt	tatcacgtga	aaatgcaaga	aacagtattt	atatacatat											ttaaaggc	1535
166	aatacagaac	cctataaaatg	gcaggttagg	gctaccatgt	aaatattttt	aatgttcata											1595
168	atgtcatagg	tggttaagtat	tttacatagc	agttactgtat	tgattattat	tgttgtcttt											1655
170	ttacccagt	acagctaaca	cacagggcat	tttttccaa	tggcaacatc	cattttgccg											1715
172	ctctgagcag	aacatttgg	tcattttatgg	catttgaacc	tgtgtctatg	agagtgccgc											1775
174	taaaaataaac	ttcctggcta	tgggtgttac	catacaacac	tggtaacctca	tgacatatga											1835
176	aaaatatgac	tcacattaaa	tcaatggat	cagttcaatg	atagttacgg	gcattaaatct											1895
178	gccaataaac	atttttagat	tttttatattt	tttttatattt	tttttatattt	tttttatattt											1955
180	tcttgtacct	tgcacat	tttgtggctag	tttatgggtc	aatagacacgc	catcatacat											2015
182	tagtcagat	aaatcgagca	ttacaaaact	caatgagcca	tagtgatgt	gacaatcaga											2075
184	agtactgtc	aagtaaatca	accatttgc	catacagatg	cacatttggaa	cagttggattc											2135
186	ttatccagaa	agggccattt	tttactatca	ctctggatt	taaatgccac	ttctaattgg											2195
188	aacttccagg	tcacaaaaat	agaatggaca	tttaaacatc	atggttctca	ttacccctaa											2255
190	taaaaactccg	tttttttttta															2274
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202	Phe	Thr	Gly	Ile	Leu	Cys	Phe	Val	Val	Ala	Arg	Gly	Val	Gly	Tyr	Tyr	
203					20				25							30	

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Input Set : A:\PH-1167US seq-revised.txt  
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205 Pro Arg Phe Ser Pro Phe Phe Leu Cys Thr His His Gly Glu Leu  
 206 35 40 45  
 208 Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala  
 209 50 55 60  
 211 Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile  
 212 65 70 75 80  
 214 Ser Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr  
 215 85 90 95  
 217 Ser Thr Ser Val Gln Ala Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe  
 218 100 105 110  
 220 Gly Phe Gly Ile Met Ser Asp Arg Gln Phe Gly Thr Gln Phe Met Cys  
 221 115 120 125  
 223 Ser Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser  
 224 130 135 140  
 226 Phe Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met  
 227 145 150 155 160  
 229 Ala Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala  
 230 165 170 175  
 232 Gln Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro  
 233 180 185 190  
 235 Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe  
 236 195 200 205  
 238 Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys  
 239 210 215 220  
 241 Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly  
 242 225 230 235 240  
 244 Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val  
 245 245 250 255  
 247 Gln Met Asn Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser  
 248 260 265 270  
 250 Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr  
 251 275 280 285  
 253 Thr Lys Asn Asn Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala  
 254 290 295 300  
 256 Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu  
 257 305 310 315 320  
 259 Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln  
 260 325 330 335  
 262 Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile  
 263 340 345 350  
 265 Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro  
 266 355 360 365  
 268 Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His  
 269 370 375 380  
 271 Thr Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Thr Glu Ser  
 272 385 390 395 400  
 274 Ser Glu Tyr Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Ser Glu  
 275 405 410 415  
 277 Asp Ile Gln Asp Gln Trp Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly

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281 <210> SEQ ID NO: 3			
282 <211> LENGTH: 2745			
283 <212> TYPE: DNA			
284 <213> ORGANISM: Mus musculus			
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287 <221> NAME/KEY: CDS			
288 <222> LOCATION: (283)..(2052)			
290 <220> FEATURE:			
291 <221> NAME/KEY: sig_peptide			
292 <222> LOCATION: (283)..(363)			
294 <220> FEATURE:			
295 <221> NAME/KEY: misc_feature			
296 <222> LOCATION: (284)..(849)			
297 <223> OTHER INFORMATION: F-spondin domain			
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300 <221> NAME/KEY: misc_feature			
301 <222> LOCATION: (970)..(1320)			
302 <223> OTHER INFORMATION: CR-50 epitope region			
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307 cccgcggccc cggcccccc cgcgtctcg ctccggccgc ccaaagtaac ttccggagcc 120			
309 tcggtctccc gctaacttcc ccccgccggc tcggttgccc ggaccggctc ggctcgagcc 180			
311 cgccgcggc tcgccttccc cgcacgcggc tcctccgtgc cggtcctcc gaaagtggat 240			
313 gagagagcgc gcggggcgcc cggcggcacg gagcgcggcg gc atg gag cgc ggc 294			
314		Met	Glu Arg Gly
315		1	
317 tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg gcg 342			
318 Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala			
319 5 10 15 20			
321 acg ctg agg gcg cgc gcg gcc acc ggc tac tac ccg cgc ttc tcg cct 390			
322 Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro Arg Phe Ser Pro			
323 25 30 35			
325 ttc ttt ttc ctg tgc acc cac cac ggg gag ctg gaa ggg gat ggg gag 438			
326 Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu			
327 40 45 50			
329 cag ggc gag gtg ctc att tcc ctg cac att gcg ggc aac ccc acc tac 486			
330 Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly Asn Pro Thr Tyr			
331 55 60 65			
333 tac gta ccg gga cag gaa tac cat gtt aca att tca aca agc acc ttc 534			
334 Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe			
335 70 75 80			
337 ttt gat ggc ttg ctg gtg acg gga ctc tat acc tcg aca agc atc cag 582			
338 Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Ile Gln			
339 85 90 95 100			
341 tct tct cag agc att gga ggc tcc agc gcc ttt gga ttc ggg atc atg 630			
342 Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Phe Gly Ile Met			
343 105 110 115			
345 tcc gac cac cag ttt ggt aac cag ttt atg tgc agt gtg gtg gcc tct 678			

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 100  
Seq#:5; N Pos. 8

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

**VERIFICATION SUMMARY**

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L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:60

L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0